Microbiology (Russian Federation) 2013 vol.82 N6, pages 668-679

Efflux systems in Serratia marcescens

Mardanova A., Bogomol'naya L., Romanova Y., Sharipova M.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

A widespread bacterium Serratia marcescens (family Enterobacteriaceae) is an opportunistic pathogen and exhibits multiple drug resistance. Active removal of antibiotics and other antimicrobials from the cells by efflux systems is one of the mechanisms responsible for microbial resistance to these compounds. Among enterobacteria, efflux systems of Escherichia coli and Salmonella enterica ser. Typhimurium have been studied most extensively. Few efflux systems that belong to different families have been reported for S. marcescens. In this review, we analyzed available literature about S. marcescens efflux systems and carried out the comparative analysis of the genes encoding the RND type systems in different Serratia species and in other enterobacteria. Bioinformatical analysis of the S. marcescens genome allowed us to identify the previously unknown efflux systems based on their homology with the relevant E. coli genes. Identification of additional efflux systems in S. marcescens genome will promote our understanding of the physiology of these bacteria, will detect new molecular mechanisms of resistance, and will reveal their resistance potential.

http://dx.doi.org/10.1134/S0026261714010093

Keywords

antibiotic resistance, bioinformatical analysis, efflux pumps, orthologous genes, Serratia marcescens